



PCT10

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,372

DATE: 11/06/2002 P.6

TIME: 15:30:16

Input Set : A:\65691270.app

Output Set: N:\CRF4\11062002\J049372.raw

3 <110> APPLICANT: PITIOT, GILLES
 4 LACAZETTE, ERIC
 5 GACHON, FRANCOISE
 7 <120> TITLE OF INVENTION: HUMAN ODORANT-BINDING PROTEINS WHICH BIND HYDROPHOBIC
 8 LIGANDS: POLYPEPTIDES AND POLYNUCLEOTIDES ENCODING SAID
 9 POLYPEPTIDES, AND USES THEREOF
 11 <130> FILE REFERENCE: 065691/0270
 13 <140> CURRENT APPLICATION NUMBER: 10/049,372
 14 <141> CURRENT FILING DATE: 2002-02-12
 16 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02319
 17 <151> PRIOR FILING DATE: 2000-08-11
 19 <150> PRIOR APPLICATION NUMBER: FR 99 10439
 20 <151> PRIOR FILING DATE: 1999-08-12
 22 <160> NUMBER OF SEQ ID NOS: 53
 24 <170> SOFTWARE: PatentIn Ver. 2.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 676
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (43)..(552)
 35 <220> FEATURE:
 36 <223> OTHER INFORMATION: cDNA396 (676) /gl (hOBPIIa-alpha)
 38 <400> SEQUENCE: 1
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 40 Met Lys Thr Leu
 41 1
 43 ttc ctg ggt gtc acg ctc ggc ctg gcc gct gcc ctg tcc acc ctg 102
 44 Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala Leu Ser Phe Thr Leu
 45 5 10 15 20
 47 gag gag gag gat atc aca ggg acc tgg tac gtg aag gcc atg gtg gtc 150
 48 Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys Ala Met Val Val
 49 25 30 35
 51 gat aag gac ttt ccg gag gac agg agg ccc agg aag gtg tcc cca gtg 198
 52 Asp Lys Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys Val Ser Pro Val
 53 40 45 50
 55 aag gtg aca gcc ctg ggc ggt ggg aac ttg gaa gcc acg ttc acc ttc 246
 56 Lys Val Thr Ala Leu Gly Gly Asn Leu Glu Ala Thr Phe Thr Phe
 57 55 60 65
 59 atg agg gag gat cgg tgc atc cag aag aaa atc ctg atg cgg aag acg 294
 60 Met Arg Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu Met Arg Lys Thr
 61 70 75 80

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63 gag gag cct ggc aaa ttc agc gcc tat ggg ggc agg aag ctc ata tac 342
64 Glu Glu Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg Lys Leu Ile Tyr
65 85 90 95 100
67 ctg cag gag ctg ccc ggg acg gac tac gtc ttt tac tgc aaa gac 390
68 Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe Tyr Cys Lys Asp
69 105 110 115
71 cag cgc cgt ggg ggc ctg cgc tac atg gga aag ctt gtg ggt agg aat 438
72 Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu Val Gly Arg Asn
73 120 125 130
75 cct aat acc aac ctg gag gcc ctg gaa gaa ttt aag aaa ttg gtg cag 486
76 Pro Asn Thr Asn Leu Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln
77 135 140 145
79 cac aag gga ctc tcg gag gag gac att ttc atg ccc ctg cag acg gga 534
80 His Lys Gly Leu Ser Glu Glu Asp Ile Phe Met Pro Leu Gln Thr Gly
81 150 155 160
83 agc tgc gtt ctc gaa cac taggcagccc ccgggtctgc acctccagag. 582.
84 Ser Cys Val Leu Glu His
85 165 170
87 cccacccatac caccagacac agagcccgga ccacctggac ctaccctcca gccatgaccc 642
89 ttccctgctc ccacccacct gactccaaat aaag. 676
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 170
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 2
98 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala Leu
99 1 5 10 15
101 Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys
102 20 25 30
104 Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys
105 35 40 45
107 Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Asn Leu Glu Ala
108 50 55 60
110 Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu
111 65 70 75 80
113 Met Arg Lys Thr Glu Glu Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg
114 85 90 95
116 Lys Leu Ile Tyr Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe
117 100 105 110
119 Tyr Cys Lys Asp Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu
120 115 120 125
122 Val Gly Arg Asn Pro Asn Thr Asn Leu Glu Ala Leu Glu Glu Phe Lys
123 130 135 140
125 Lys Leu Val Gln His Lys Gly Leu Ser Glu Glu Asp Ile Phe Met Pro
126 145 150 155 160
128 Leu Gln Thr Gly Ser Cys Val Leu Glu His
129 165 170
132 <210> SEQ ID NO: 3
133 <211> LENGTH: 725

RAW SEQUENCE LISTING
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Input Set : A:\65691270.app
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134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapiens
137 <220> FEATURE:
138 <221> NAME/KEY: CDS
139 <222> LOCATION: (43)..(480)
141 <220> FEATURE:
142 <223> OTHER INFORMATION: cDNA396 (725) /SM12 (hOBPIIa-beta)
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146 Met Lys Thr Leu
147 1
149 ttc ctg ggt gtc acg ctc ggc ctg gcc gct gcc ctg tcc ttc acc ctg 102
150 Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala Leu Ser Phe Thr Leu
151 5 10 15 20
153 gag gag gag gat atc aca ggg acc tgg tac gtg aag gcc atg gtg gtc 150
154 Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys Ala Met Val Val
155 25 30 35
157 gat aag gac ttt ccg gag gac agg agg ccc agg aag gtg tcc cca gtg 198
158 Asp Lys Asp Phe Pro Glu Asp Arg Pro Arg Lys Val Ser Pro Val
159 40 45 50
161 aag gtg aca gcc ctg ggc ggt ggg aac ttg gaa gcc acg ttc acc ttc 246
162 Lys Val Thr Ala Leu Gly Gly Asn Leu Glu Ala Thr Phe Thr Phe
163 55 60 65
165 atg agg gag gat cgg tgc atc cag aag aaa atc ctg atg cgg aag acg 294
166 Met Arg Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu Met Arg Lys Thr
167 70 75 80
169 gag gag cct ggc aaa ttc agc gcc tat ggg ggc agg aag ctc ata tac 342
170 Glu Glu Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg Lys Leu Ile Tyr
171 85 90 95 100
173 ctg cag gag ctg ccc ggg acg gac gac tac gtc ttt tac tgc aaa gac 390
174 Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe Tyr Cys Lys Asp
175 105 110 115
177 cag cgc cgt ggg ggc ctg cgc tac atg gga aag ctt gtg ggg ccc tgc 438
178 Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu Val Gly Pro Cys
179 120 125 130
181 cgc tgt ccc cac gtc ggc tca cct ggc cac ctc acc tgc agg 480
182 Arg Cys Pro His Val Gly Ser Pro Gly His Leu Thr Cys Arg
183 135 140 145
185 taggaatctt aataccaaacc tggaggccct ggaagaattt aagaaatgg tgcagcacaa 540
187 gggactctcg gaggaggaca tttcatgcc cctgcagacg ggaagctcg ttctcgaaca 600
189 ctaggcaggcc cccgggtctg cacctccaga gcccaccccta ccaccagaca cagagcccg 660
191 accacaccttga cctaccctcc agccatgacc cttccctgct cccacccacc tgactccaaa 720
193 taaag 725
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 146
198 <212> TYPE: PRT
199 <213> ORGANISM: Homo sapiens
201 <400> SEQUENCE: 4
202 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Leu

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/049,372DATE: 11/06/2002
TIME: 15:30:16Input Set : A:\65691270.app
Output Set: N:\CRF4\11062002\J049372.raw

203	1	5	10	15														
205	Ser	Phe	Thr	Leu	Glu	Glu	Glu	Asp	Ile	Thr	Gly	Thr	Trp	Tyr	Val	Lys		
206				20						25				30				
208	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg	Pro	Arg	Lys		
209					35					40				45				
211	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly	Asn	Leu	Glu	Ala		
212					50				55				60					
214	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile	Gln	Lys	Lys	Ile	Leu		
215					65				70			75			80			
217	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Phe	Ser	Ala	Tyr	Gly	Gly	Arg		
218						85				90				95				
220	Lys	Leu	Ile	Tyr	Leu	Gln	Glu	Leu	Pro	Gly	Thr	Asp	Asp	Tyr	Val	Phe		
221						100			105				110					
223	Tyr	Cys	Lys	Asp	Gln	Arg	Arg	Gly	Gly	Leu	Arg	Tyr	Met	Gly	Lys	Leu		
224						115			120				125					
226	Val	Gly	Pro	Cys	Arg	Cys	Pro	His	Val	Gly	Ser	Pro	Gly	His	Leu	Thr		
227						130			135				140					
229	Cys	Arg																
230	145																	
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235	<211>	LENGTH:	741															
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239	<220>	FEATURE:																
240	<221>	NAME/KEY:	CDS															
241	<222>	LOCATION:	(43)..(726)															
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249														1				
251	ttc	ctg	ggc	acg	ctc	ggc	ctg	gct	gcc	ctg	tcc	ttc	acc	ctg				
252	Phe	Leu	Gly	Val	Thr	Leu	Gly	Leu	Ala	Ala	Ala	Leu	Ser	Phe	Thr	Leu		
253						5		10			15			20				
255	gag	gag	gag	gat	atc	aca	ggg	acc	tgg	tac	gtg	aag	gcc	atg	gtg	gtc		
256	Glu	Glu	Glu	Asp	Ile	Thr	Gly	Thr	Trp	Tyr	Val	Lys	Ala	Met	Val	Val		
257							25			30			35					
259	gat	aag	gac	ttt	ccg	gag	gac	agg	ccc	agg	aag	gtg	tcc	cca	gtg			
260	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg	Pro	Arg	Lys	Val	Ser	Pro	Val		
261							40			45			50					
263	aag	gtg	aca	gcc	ctg	ggc	ggt	ggg	aac	ttg	gaa	gcc	acg	ttc	acc	ttc		
264	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly	Asn	Leu	Gly	Ala	Thr	Phe	Thr	Phe		
265						55			60			65						
267	atg	agg	gag	gat	cg	tgc	atc	cag	aaa	atc	ctg	atg	cg	aag	acg			
268	Met	Arg	Glu	Asp	Arg	Cys	Ile	Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr		
269						70			75			80						
271	gag	gag	cct	ggc	aaa	ttc	agc	gcc	tat	ggg	ggc	agg	aag	ctc	ata	tac		
272	Glu	Glu	Pro	Gly	Lys	Phe	Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Ile	Tyr		

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273	85	90	95	100
275	ctg cag gag ctg ccc ggg acg gac gac tac gtc ttt tac tgc aaa gac			390
276	Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe Tyr Cys Lys Asp			
277	105	110	115	
279	cag cgc cgt ggg ggc ctg cgc tac atg gga aag ctt gtg gca tct gct			438
280	Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu Val Ala Ser Ala			
281	120	125	130	
283	ccc tgc agg gcc gtg ccg ctg tcc cca cgt cgg ctc acc tgg cca cct			486
284	Pro Cys Arg Ala Val Pro Leu Ser Pro Arg Arg Leu Thr Trp Pro Pro			
285	135	140	145	
287	cac ctg cag gta gga atc cta ata cca acc tgg agg ccc tgg aag aat			534
288	His Leu Gln Val Gly Ile Leu Ile Pro Thr Trp Arg Pro Trp Lys Asn			
289	150	155	160	
291	tta aga aat tgg tgc agc aca agg gac tct cgg agg agg aca ttt tca			582
292	Leu Arg Asn Trp Cys Ser Thr Arg Asp Ser Arg Arg Arg Thr Phe Ser			
293	165	170	175	180
295	tgc ccc tgc aga cgg gaa gct gcg ttc tcg aac act agg cag ccc cgg			630
296	Cys Pro Cys Arg Arg Glu Ala Ala Phe Ser Asn Thr Arg Gln Pro Pro			
297	185	190	195	
299	ggc ctg cac ctc cag agc cca ccc tac cac cag aca cag agc ccg gac			678
300	Gly Leu His Leu Gln Ser Pro Pro Tyr His Gln Thr Gln Ser Pro Asp			
301	200	205	210	
303	cac ctg gac cta ccc tcc agc cat gac cct tcc ctg ctc cca ccc acc			726
304	His Leu Asp Leu Pro Ser Ser His Asp Pro Ser Leu Leu Pro Pro Thr			
305	215	220	225	
307	tgactccaaa taaag			741
310	<210> SEQ ID NO: 6			
311	<211> LENGTH: 228			
312	<212> TYPE: PRT			
313	<213> ORGANISM: Homo sapiens			
315	<400> SEQUENCE: 6			
316	Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala Leu			
317	1	5	10	15
319	Ser Phe Thr Leu Glu Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys			
320	20	25	30	
322	Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys			
323	35	40	45	
325	Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala			
326	50	55	60	
328	Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu			
329	65	70	75	80
331	Met Arg Lys Thr Glu Glu Pro Gly Lys Phe Ser Ala Tyr Gly Arg			
332	85	90	95	
334	Lys Leu Ile Tyr Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe			
335	100	105	110	
337	Tyr Cys Lys Asp Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu			
338	115	120	125	
340	Val Ala Ser Ala Pro Cys Arg Ala Val Pro Leu Ser Pro Arg Arg Leu			
341	130	135	140	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/06/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 8507,10635,10643

VERIFICATION SUMMARY

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Input Set : A:\65691270.app

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L:919 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:8460

L:955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:10620